SEQUENCE LISTING

<110> AZPIROZ, Ricardo
CHOE, Sunghwa
FELDMANN, Kenneth

<120> DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF

<130> 2225-0001

<140> 09/502,426
<141> 2000-02-11

<150> 60/119,657
<151> 1999-02-11

<150> 60/119,658
<151> 1999-02-11

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 6888
<212> DNA
<213> Arabidopsis sp.

<400> 1
atgtgggtat tatattgttg ggttcggttt gagctacaat ataaatttcg tgtttctggt 60
tattctgttc acatgatttg agtttggttc tcaatttgga ttccaagata attaaatatt 120
aaaattcatt taaaatattt acaagtaatt aattatcttt acattgtatt gttataacaa 180
aatatctatc tttggtatat gagaaaatat ggagtttgga atttataata ataaaggaaa 240
taatcgattc catttggttg gattacacag ttaagttttt gtgtttcttt tgttatatgt 300
atatgagtaa atcaaaaaga gtattgattg aagtgtaaac atatttcgtt atgaccccca 360
aaaaaaaaaa aaaaacaaac aaacaaaccc ccccccccgat atagtttttg gttctggatt 420
aggtttattt gatcataatt acatgcatca tttctttgat tactatgaag attttcttac 480
caattaaaat ttcgaattca tatctcttga ttattaaatt aaatacgagt gtgaatatcc 540
gtttatcgat cactccaatc atgattatga ttcttgtgct aatccagcaa attattaaca 600
agagtattga gaaaaaaccg aaaataagaa aagggaaaga gtagtgaccc atggagtatg 660
tgaataatta tcaaagagaa taagagatga caaccaaaag gttgtggaat aatggtccct 720
gccagctttc tctcacaatc aatatcgacc ctatttggat tttctggata ttcgttaaaa 780
tttgcgataa cgattgtgaa aaatatttta tttgttagct gatctcaata ttatgttcca 840
ggtatttgca taatcttctg tttaaagcat attttgtctt tctttttgtt tcgtttctct 900
taactatata ttatcgcgga tatatgataa caatgatata tcacaaaaca attgtctggg 960
accattttga ataaactttt tctcaaacat tacgggacac tggactcgac ccttaaaata 1020
cgattttaca gcgtcactag ttgagattac tagcataaag cataaaggac ccgttcaagc 1080
tatttataca aagttacaaa ctgaatatag cttgaaatcc tttagaaaat tttggaatta 1140
ccggttgtta tgtaaatata gatttagtgg taaacaaata tgttaatcaa ttagtggtca 1200
acatatacat aattccttac agaaaaaaca aacttaagag aagttaacat atccatatat 1260
gggtatgcta tacctttcac gtatgctata ctagagacta aagaatagtt atgtgatgtc 1320
gataaatgaa attcacacgc gtggtaataa ttatgggacc gtatgttacg atcactgcaa 1380
atatcattct tggttggtca acaataaaaa caaaaacaag aaaaaaagaa aacgattttt 1440
cttggattcc attcaatgat ctaaaatgca tagatctttt gggttacagt ttcgaagtcc 1500
tctacaagcg tgtaaccatc tgcaactatt aaattgcttt ctttaatgca tctttaacat 1560
atttattgtt agttggaatt taataagagc gaacttgtaa cattacaata tttatattag 1620

atactagtat gtgattattc caaatacata ctttggatgt ttaaacttaa tcttgtttct 1680
tcctacggta taaatattaa tcatcgaggt aaaaaaagtt ttgtcttatt ttcgcgatgc 1740
atgaaggata aacctaatga ctttaatttt ttgaaaatgt aacccttta ctcatagatt 1800
aattaccgta tgtttttgtt gccataatga cagcctctac aactgtgata gtcaattttt 1860
tctgcaaata ttaaattagg aattcaatgc tactatcaat agaagaaaca gctgagtatt 1920
acattttaat ttaaagacaa aatttttgaa aaatgttata atttctaaca atattattaa 1980
aatatgatgc ctataatgta tttcctatgt tcttaaaata tttttttta tatttagtta 2040
taaatacatt atgaaccaat aatagttggt gaattcaaat atctccatta atatttttg 2100
aaatctacaa attattaata tttagtcaat aacaatgcat agaaagttcc aaaaaaaatt 2160
ttgttaacag aaacttccaa attttttttt tttatggaac aagaaataac agatagaaaa 2220
ctattttgtt gtggaatgga agtagtaata tacattaagc aaattttaaa aaattatata 2280
agcctatacg cgctcaaagt atgttatcta gtaggtgtaa ttaataatgc atggtgcgat 2340
tcagaattgg gacaacaatg aaaacggaat taaaatatta actttaaaat aaataaaaat 2400
ttgagtaaat gtgttttctg actattgagg ggcaaaaaaa agacaatgcc aaaagtctac 2460
gggtttgact gtccagttcg gtaataatct aataactctg tctttgaccg cacgctcgtg 2520
taggggtcct tctgacattt tcactgttct acccctactc gtgagcccac ccttttccca 2580
tatcctaagg gtaattttgg aaatcccaat ttaaaccgat tgagaccgta ccggacttcc 2640
tgggattctg ctggagcatt tatcaaaaat tattagcacg aatgggttta ttaatttaaa 2700
aactcacaac ttgatcagat aaaatttcat aaacactttt acgatggatt cgtacgatct 2760
atctaatgac ttttttttt ctaccacggt ggatgaaagt tatagtacta ttagccagag 2820
acaattgatt atagatatat ccattaatcc atgatattta tgatataaat agctgttaaa 2880
ctatttcagc atcgcagctt tctgcaactt ttgtttttaa tttaagagtt taataaataa 2940
aagtattaaa aggagcataa cgaggcaaca aaagtaatga acacggagaa acaaaagcca 3000
tgaagctcat tggttagttt aagcttaata agaagatttt attaaatttt aatgacgatg 3060
ataacaatta tattttctga cttctttaaa acccccctct acaaacagaa gctccctttt 3120
tcagtagaag tccgattccc aatcttaaag acaaagccat tagaaagaga aagtgagtga 3180
gagagagaga gaaactagct ccatgttcga aacagagcat catactctct tacctcttct 3240
tcttctccca tcgcttttgt ctcttcttct cttcttgatt ctcttgaaga gaagaaatag 3300
aaaaaccaga ttcaatctac ctccgggtaa atccggttgg ccatttcttg gtgaaaccat 3360
cggttatctt aaaccgtaca ccgccacaac actcggtgac ttcatgcaac aacatgtctc 3420
caagtaaaca acaacatctt ccaaaaactc aaaaaaataa atcctctgtt tttgaaattt 3480
gactaatgtt gtttatttta caggtatggt aagatatata gatcgaactt gtttggagaa 3540
ccaacgatcg tatcagctga tgctggactt aatagattca tattacaaaa cgaaggaagg 3600
ctctttgaat gtagttatcc tagaagtata ggtgggattc ttgggaaatg gtcgatgctt 3660
gttcttgttg gtgacatgca tagagatatg agaagtatct cgcttaactt cttaagtcac 3720
gcacgtctta gaactattct acttaaagat gttgagagac atactttgtt tgttcttgat 3780
tcttggcaac aaaactctat tttctctgct caagacgagg ccaaaaaggt ttttatttt 3840
atcttttatt ttgctaaatt tttttgttta tgaatcttta gagtttctaa ctttttttt 3900
tttaattgaa cagtttacgt ttaatctaat ggcgaagcat ataatgagta tggatcctgg 3960
agaagaagaa acagagcaat taaagaaaga gtatgtaact ttcatgaaag gagttgtctc 4020
tgctcctcta aatctaccag gaactgctta tcataaagct cttcaggtac atttatttt 4080
ttttgctgta aagtcacaaa ctctcattat aggtttttaa ttttatttta tgtgttaaat 4140
aaaatatcta aaatggttgt gtagtcacga gcaacgatat tgaagttcat tgagaggaaa 4200
atggaagaga gaaaattgga tatcaaggaa gaagatcaag aagaagaaga agtgaaaaca 4260
gaggatgaag cagagatgag taagagtgat catgttagga aacaaagaac agacgatgat 4320
cttttgggat gggttttgaa acattcgaat ttatcgacgg agcaaattct cgatctcatt 4380
cttagtttgt tatttgccgg acatgagact tcttctgtag ccattgctct cgctatcttc 4440
ttcttgcaag cttgccctaa agccgttgaa gagcttaggg taagataatt ataacagcac 4500
aagttaatta ctaccaaatt gttacgtatt atataagtta ttatagaatt attctattag 4560
aatatacgat gaaaaaagta tgtatattta attgtcacta attttatgtt tattgattta 4620
tacttttgaa ggaagagcat cttgagatcg cgagggccaa gaaggaacta ggagagtcag 4680
aattaaattg ggatgattac aagaaaatgg actttactca atgtgtatgt tactatcatt 4740
ctcattattt attctatgtt catatgattt atgatgaaac caaaattatt gatttttttt 4800
ttggtgtgtg tgaaggttat aaatgaaact cttcgattgg gaaatgtagt taggtttttg 4860
catcgcaaag cactcaaaga tgttcggtac aaaggtaaaa ctttacgtac aaaatttta 4920
aataatgaaa tccggaatat tgaaatctta ttggatgaaa aatattaaaa taatttacat 4980
ttcttaatgt tggaaaaaag gatacgatat ccctagtggg tggaaagtgt taccggtgat 5040

```
ctcagccgta catttggata attctcgtta tgaccaacct aatctcttta atccttggag 5100
atggcaacag gtaaataaaa agtttctctc gttaactatc gaaaattagt gtatagtttt 5160
ttcatctatt gcatgaatag atacgtccta cgtgatttac ctatctatag atactatacg 5220
agaactatta atctggcaaa aacttttttat tattattatc tttcaagtta gatcttaaca 5280
cgtcatggat cattgatcac atgaaagcat ataaattaaa aataagagag agaaagagac 5340
gtgttggtgt aagtgtacgt gaagacaatt aattagtagg atggtatgtc tttaatgacg 5400
taggagctgc ctaaatattc ttataatcgt gaccgttgat ttattattag tcacggcttt 5460
gatacaattt aagatttgac ggacgatggt accacggctt tgacggatct cacacgcccg 5520
atgacttgta cgtgcgttag attctgccac gttgactggt tttaatactt agatttataa 5580
ctctattaat tataacaact atcaaatcgg cgaattagag aaatatacta tatagtatta 5640
ttatgattat tatgagataa tactttatga aataagataa taatggtagt catgatgtta 5700
tagtgagtgg ggaaggtaag aggtggtgag agatgattaa tgaccccacg tggtgtggtg 5760
ccaacaagca cgtgttcttc ttccttttt cttcccaact tctttttttg ggggtttatt 5820
gtgatttata aaatcggttt gtcgtttttt tttgtgacga gcagcaaaac aacggagcgt 5880
catcgtcagg aagtggtagt ttttcgacgt ggggaaacaa ctacatgccg tttggaggag 5940
ggccaaggct atgtgctggt tcagagctag ccaagttaga aatggcagtg tttattcatc 6000
atctagttct taaattcaat tgggaattag cagaagatga tcaaccattt gcttttcctt 6060
ttgttgattt tcctaacggt ttgcctatta gggtttctcg tattctgtaa aaaaaaaaaa 6120
agatgaaagt atttttattc tcttcttttt tttttgataa ttttaaatca tttttttttgc 6180
ccaatgatat ataaaaattt ggataaataa tattattgga tattcgtttt ttagttcggg 6240
tttgagaaaa gggtttcgac tttcgaaagt ggacgatgta tatagattgg gagctaggtt 6300
gagtctttgg acatttgtat tggatgttgt tgattattag tgtcgacact attaaacctt 6360
aaatgggctt tctataaggc ccaattatat tacgattata acaaagtgac aacttttact 6420
tcgtttttga tccgaagcaa taacaaattg tcaaatacca aacacaagaa ttatgtaaac 6480
actcgtgtgt gtctagtggg aaatcattgg gctggagact gaacatcaga acacaagaaa 6540
cctgtcaatt atggatacac ctcctatgac ggtttccaaa ctttatcttg attcttatcg 6600
tgttacattg acacaaagag ttaggtgtca aaaggactaa atgaataaca atagctctca 6660
ggataagaag gttcataaaa tggtttcttt attttgagaa gaaagagaga ggagctttta 6720
ctgtttcttg ggtcctattc ctttaaatga gagggtttcg tttttacttc ttctatctca 6780
tcatctttag gatcctcttc tagacgagta aagtaatcct cgttaccaag caatggtctc 6840
atcttttgaa gacaggtctt ttccaagtcc tagttcaggc caaagctt              6888
```

<210> 2
<211> 513
<212> PRT
<213> Arabidopsis sp.

<400> 2

```
Met Phe Glu Thr Glu His His Thr Leu Leu Pro Leu Leu Leu Leu Pro
  1               5                  10                  15

Ser Leu Leu Ser Leu Leu Leu Phe Leu Ile Leu Leu Lys Arg Arg Asn
             20                  25                  30
Arg Lys Thr Arg Phe Asn Leu Pro Pro Gly Lys Ser Gly Trp Pro Phe
         35                  40                  45

Leu Gly Glu Thr Ile Gly Tyr Leu Lys Pro Tyr Thr Ala Thr Thr Leu
     50                  55                  60

Gly Asp Phe Met Gln Gln His Val Ser Lys Tyr Gly Lys Ile Tyr Arg
 65                  70                  75                  80

Ser Asn Leu Phe Gly Glu Pro Thr Ile Val Ser Ala Asp Ala Gly Leu
                85                  90                  95

Asn Arg Phe Ile Leu Gln Asn Glu Gly Arg Leu Phe Glu Cys Ser Tyr
            100                 105                 110
```

```
Pro Arg Ser Ile Gly Gly Ile Leu Gly Lys Trp Ser Met Leu Val Leu
        115                 120                 125

Val Gly Asp Met His Arg Asp Met Arg Ser Ile Ser Leu Asn Phe Leu
    130                 135                 140

Ser His Ala Arg Leu Arg Thr Ile Leu Leu Lys Asp Val Glu Arg His
145                 150                 155                 160

Thr Leu Phe Val Leu Asp Ser Trp Gln Gln Asn Ser Ile Phe Ser Ala
                165                 170                 175

Gln Asp Glu Ala Lys Lys Phe Thr Phe Asn Leu Met Ala Lys His Ile
            180                 185                 190

Met Ser Met Asp Pro Gly Glu Glu Glu Thr Glu Gln Leu Lys Lys Glu
        195                 200                 205

Tyr Val Thr Phe Met Lys Gly Val Val Ser Ala Pro Leu Asn Leu Pro
    210                 215                 220

Gly Thr Ala Tyr His Lys Ala Leu Gln Ser Arg Ala Thr Ile Leu Lys
225                 230                 235                 240

Phe Ile Glu Arg Lys Met Glu Glu Arg Lys Leu Asp Ile Lys Glu Glu
                245                 250                 255

Asp Gln Glu Glu Glu Glu Val Lys Thr Glu Asp Glu Ala Glu Met Ser
            260                 265                 270

Lys Ser Asp His Val Arg Lys Gln Arg Thr Asp Asp Asp Leu Leu Gly
        275                 280                 285

Trp Val Leu Lys His Ser Asn Leu Ser Thr Glu Gln Ile Leu Asp Leu
    290                 295                 300

Ile Leu Ser Leu Leu Phe Ala Gly His Glu Thr Ser Ser Val Ala Ile
305                 310                 315                 320

Ala Leu Ala Ile Phe Phe Leu Gln Ala Cys Pro Lys Ala Val Glu Glu
                325                 330                 335

Leu Arg Glu Glu His Leu Glu Ile Ala Arg Ala Lys Lys Glu Leu Gly
            340                 345                 350

Glu Ser Glu Leu Asn Trp Asp Asp Tyr Lys Lys Met Asp Phe Thr Gln
        355                 360                 365

Cys Val Ile Asn Glu Thr Leu Arg Leu Gly Asn Val Val Arg Phe Leu
    370                 375                 380

His Arg Lys Ala Leu Lys Asp Val Arg Tyr Lys Gly Tyr Asp Ile Pro
385                 390                 395                 400

Ser Gly Trp Lys Val Leu Pro Val Ile Ser Ala Val His Leu Asp Asn
                405                 410                 415
```

Ser Arg Tyr Asp Gln Pro Asn Leu Phe Asn Pro Trp Arg Trp Gln Gln
420 425 430

Gln Asn Asn Gly Ala Ser Ser Ser Gly Ser Gly Ser Phe Ser Thr Trp
435 440 445

Gly Asn Asn Tyr Met Pro Phe Gly Gly Gly Pro Arg Leu Cys Ala Gly
450 455 460

Ser Glu Leu Ala Lys Leu Glu Met Ala Val Phe Ile His His Leu Val
465 470 475 480

Leu Lys Phe Asn Trp Glu Leu Ala Glu Asp Asp Gln Pro Phe Ala Phe
485 490 495

Pro Phe Val Asp Phe Pro Asn Gly Leu Pro Ile Arg Val Ser Arg Ile
500 505 510

Leu

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4OVERF

<400> 3
atgttcgaaa cagagcatca tact 24

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4PRM

<400> 4
cctcgatcaa agagagagag a 21

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4RTF

<400> 5
ttcttggtga aaccatcggt tatcttaaa 29

<210> 6
<211> 26

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4RTR

<400> 6
tatgataagc agttcctggt agattt 26

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4F1

<400> 7
cgaggcaaca aaagtaatga a 21

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4R1

<400> 8
gttagaaact ctaaagattc a 21

<210> 9
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4F2

<400> 9
gattcttggc aacaaaactc tat 23

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4R2

<400> 10
ccgaacatct ttgagtgctt 20

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4F3

<400> 11
gtgtgaaggt tataaatgaa actctt 26

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4R3

<400> 12
ggtttaatag tgtcgacact aata 24

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4F4

<400> 13
ccgatgactt gtacgtgcgt ta 22

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4F5

<400> 14
gcgaagcata taatgagtat ggat 24

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D4R5

<400> 15
gttggtcata acgagaatta tccaaa 26

<210> 16
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer D4XLINIT

<400> 16
taggatccag ctagtttctc tctctctct 29

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer T7

<400> 17
taatacgact cactataggg 20

<210> 18
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
D4OVERFA

<400> 18
gaattctaga atgttcgaaa cagagcatca ta 32

<210> 19
<211> 472
<212> PRT
<213> Arabidopsis thaliana

<400> 19

```
Met Ala Phe Thr Ala Phe Leu Leu Leu Leu Ser Ser Ile Ala Ala Gly
 1               5                  10                  15
Phe Leu Leu Leu Leu Arg Arg Thr Arg Tyr Arg Arg Met Gly Leu Pro
            20                  25                  30
Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr Phe Gln Leu Ile
        35                  40                  45
Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile Asp Glu Arg Val
    50                  55                  60
Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe Gly Glu Pro Thr
65                  70                  75                  80
Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val Leu Gln Asn Glu
                85                  90                  95
Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile Cys Asn Leu Leu
            100                 105                 110
Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu His Lys Arg Met
        115                 120                 125
His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile Ile Lys Asp His
    130                 135                 140
Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn Leu Asp Ser Trp
145                 150                 155                 160
Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys Ile Thr Phe Glu
                165                 170                 175
Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly Glu Trp Ser Glu
```

```
            180                 185                 190
Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly Phe Phe Ser Leu
        195                 200                 205
Pro Leu Pro Leu Phe Ser Thr Thr Tyr Arg Lys Ala Ile Gln Ala Arg
    210                 215                 220
Arg Lys Val Ala Glu Ala Leu Thr Val Val Val Met Lys Arg Arg Glu
225                 230                 235                 240
Glu Glu Glu Glu Gly Ala Glu Arg Lys Lys Asp Met Leu Ala Ala Leu
                245                 250                 255
Leu Ala Ala Asp Asp Gly Phe Ser Asp Glu Glu Ile Val Asp Phe Leu
            260                 265                 270
Val Ala Leu Leu Val Ala Gly Tyr Glu Thr Thr Ser Thr Ile Met Thr
        275                 280                 285
Leu Ala Val Lys Phe Leu Thr Glu Thr Pro Leu Ala Leu Ala Gln Leu
    290                 295                 300
Lys Glu Glu His Glu Lys Ile Arg Ala Met Lys Ser Asp Ser Tyr Ser
305                 310                 315                 320
Leu Glu Trp Ser Asp Tyr Lys Ser Met Pro Phe Thr Gln Cys Val Val
                325                 330                 335
Asn Glu Thr Leu Arg Val Ala Asn Ile Ile Gly Gly Val Phe Arg Arg
            340                 345                 350
Ala Met Thr Asp Val Glu Ile Lys Gly Tyr Lys Ile Pro Lys Gly Trp
        355                 360                 365
Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp Pro Asn His Phe
    370                 375                 380
Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln Ser Asn Ser Val
385                 390                 395                 400
Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly Gly Gly Pro Arg
                405                 410                 415
Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu Ser Val Phe Leu
            420                 425                 430
His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala Glu Gln Asp Lys
        435                 440                 445
Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg Tyr Pro Ile Phe
    450                 455                 460
Val Lys Arg Arg Asp Phe Ala Thr
465                 470
```

<210> 20
<211> 464
<212> PRT
<213> Lycopersicon esculentum

<400> 20

```
Met Ala Phe Phe Leu Ile Phe Leu Ser Ser Phe Phe Gly Leu Cys Ile
 1               5                  10                  15
Phe Cys Thr Ala Leu Leu Arg Trp Asn Gln Val Lys Tyr Asn Gln Lys
            20                  25                  30
Asn Leu Pro Pro Gly Thr Met Gly Trp Pro Leu Phe Gly Glu Thr Thr
        35                  40                  45
Glu Phe Leu Lys Leu Gly Pro Ser Phe Met Lys Asn Gln Arg Ala Arg
    50                  55                  60
Tyr Gly Ser Phe Phe Lys Ser His Ile Leu Gly Cys Pro Thr Ile Val
65                  70                  75                  80
Ser Met Asp Ser Glu Leu Asn Arg Tyr Ile Leu Val Asn Glu Ala Lys
                85                  90                  95
Gly Leu Val Pro Gly Tyr Pro Gln Ser Met Ile Asp Ile Leu Gly Lys
```

```
            100                 105                 110
Cys Asn Ile Ala Ala Val Asn Gly Ser Ala His Lys Tyr Met Arg Gly
        115                 120                 125
Ala Leu Leu Ser Leu Ile Ser Pro Thr Met Ile Arg Asp Gln Leu Leu
    130                 135                 140
Pro Lys Ile Asp Glu Phe Met Arg Ser His Leu Thr Asn Trp Asp Asn
145                 150                 155                 160
Lys Val Ile Asp Ile Gln Glu Lys Thr Asn Lys Met Ala Phe Leu Ser
                165                 170                 175
Ser Leu Lys Gln Ile Ala Gly Ile Glu Ser Thr Ser Leu Ala Gln Glu
            180                 185                 190
Phe Met Ser Glu Phe Phe Asn Leu Val Leu Gly Thr Leu Ser Leu Pro
        195                 200                 205
Ile Asn Leu Pro Asn Thr Asn Tyr His Arg Gly Phe Gln Ala Arg Lys
    210                 215                 220
Ile Ile Val Asn Leu Leu Arg Thr Leu Ile Glu Glu Arg Arg Ala Ser
225                 230                 235                 240
Lys Glu Ile Gln His Asp Met Leu Gly Tyr Leu Met Asn Glu Glu Ala
                245                 250                 255
Thr Arg Phe Lys Leu Thr Asp Asp Glu Met Ile Asp Leu Ile Ile Thr
            260                 265                 270
Ile Leu Tyr Ser Gly Tyr Glu Thr Val Ser Thr Thr Ser Met Met Ala
        275                 280                 285
Val Lys Tyr Leu His Asp His Pro Lys Val Leu Glu Glu Leu Arg Lys
    290                 295                 300
Glu His Met Ala Ile Arg Glu Lys Lys Lys Pro Glu Asp Pro Ile Asp
305                 310                 315                 320
Tyr Asn Asp Tyr Arg Ser Met Arg Phe Thr Arg Ala Val Ile Leu Glu
                325                 330                 335
Thr Ser Arg Leu Ala Thr Ile Val Asn Gly Val Leu Arg Lys Thr Thr
            340                 345                 350
Gln Asp Met Glu Ile Asn Gly Tyr Ile Ile Pro Lys Gly Trp Arg Ile
        355                 360                 365
Tyr Val Tyr Thr Arg Glu Leu Asn Tyr Asp Pro Arg Leu Tyr Pro Asp
    370                 375                 380
Pro Tyr Ser Phe Asn Pro Trp Arg Trp Met Asp Lys Ser Leu Glu His
385                 390                 395                 400
Gln Asn Ser Phe Leu Val Phe Gly Gly Gly Thr Arg Gln Cys Pro Gly
                405                 410                 415
Lys Glu Leu Gly Val Ala Glu Ile Ser Thr Phe Leu His Tyr Phe Val
            420                 425                 430
Thr Lys Tyr Arg Trp Glu Glu Ile Gly Gly Asp Lys Leu Met Lys Phe
        435                 440                 445
Pro Arg Val Glu Ala Pro Asn Gly Leu Arg Ile Arg Val Ser Ala His
    450                 455                 460

<210> 21
<211> 444
<212> PRT
<213> Synechocystis sp.

<400> 21
Met Ile Thr Ser Pro Thr Asn Leu Asn Ser Leu Pro Ile Pro Pro Gly
 1               5                  10                  15
Asp Phe Gly Leu Pro Trp Leu Gly Glu Thr Leu Asn Phe Leu Asn Asp
            20                  25                  30
Gly Asp Phe Gly Lys Lys Arg Gln Gln Gln Phe Gly Pro Ile Phe Lys
```

```
        35                  40                  45
Thr Arg Leu Phe Gly Lys Asn Val Ile Phe Ile Ser Gly Ala Leu Ala
    50                  55                  60
Asn Arg Phe Leu Phe Thr Lys Glu Gln Glu Thr Phe Gln Ala Thr Trp
65                  70                  75                  80
Pro Leu Ser Thr Arg Ile Leu Leu Gly Pro Asn Ala Leu Ala Thr Gln
                85                  90                  95
Met Gly Glu Ile His Arg Ser Arg Arg Lys Ile Leu Tyr Gln Ala Phe
            100                 105                 110
Leu Pro Arg Thr Leu Asp Ser Tyr Leu Pro Lys Met Asp Gly Ile Val
        115                 120                 125
Gln Gly Tyr Leu Glu Gln Trp Gly Lys Ala Asn Glu Val Ile Trp Tyr
    130                 135                 140
Pro Gln Leu Arg Arg Met Thr Phe Asp Val Ala Ala Thr Leu Phe Met
145                 150                 155                 160
Gly Glu Lys Val Ser Gln Asn Pro Gln Leu Phe Pro Trp Phe Glu Thr
                165                 170                 175
Tyr Ile Gln Gly Leu Phe Ser Leu Pro Ile Pro Leu Pro Asn Thr Leu
            180                 185                 190
Phe Gly Lys Ser Gln Arg Ala Arg Ala Leu Leu Leu Ala Glu Leu Glu
        195                 200                 205
Lys Ile Ile Lys Ala Arg Gln Gln Gln Pro Pro Ser Glu Glu Asp Ala
    210                 215                 220
Leu Gly Ile Leu Leu Ala Ala Arg Asp Asp Asn Asn Gln Pro Leu Ser
225                 230                 235                 240
Leu Pro Glu Leu Lys Asp Gln Ile Leu Leu Leu Leu Phe Ala Gly His
                245                 250                 255
Glu Thr Leu Thr Ser Ala Leu Ser Ser Phe Cys Leu Leu Leu Gly Gln
            260                 265                 270
His Ser Asp Ile Arg Glu Arg Val Arg Gln Glu Gln Asn Lys Leu Gln
        275                 280                 285
Leu Ser Gln Glu Leu Thr Ala Glu Thr Leu Lys Lys Met Pro Tyr Leu
    290                 295                 300
Asp Gln Val Leu Gln Glu Val Leu Arg Leu Ile Pro Pro Val Gly Gly
305                 310                 315                 320
Gly Phe Arg Glu Leu Ile Gln Asp Cys Gln Phe Gln Gly Phe His Phe
                325                 330                 335
Pro Lys Gly Trp Leu Val Ser Tyr Gln Ile Ser Gln Thr His Ala Asp
            340                 345                 350
Pro Asp Leu Tyr Pro Asp Pro Glu Lys Phe Asp Pro Glu Arg Phe Thr
        355                 360                 365
Pro Asp Gly Ser Ala Thr His Asn Pro Pro Phe Ala His Val Pro Phe
    370                 375                 380
Gly Gly Gly Leu Arg Glu Cys Leu Gly Lys Glu Phe Ala Arg Leu Glu
385                 390                 395                 400
Met Lys Leu Phe Ala Thr Arg Leu Ile Gln Gln Phe Asp Trp Thr Leu
                405                 410                 415
Leu Pro Gly Gln Asn Leu Glu Leu Val Val Thr Pro Ser Pro Arg Pro
            420                 425                 430
Lys Asp Asn Leu Arg Val Lys Leu His Ser Leu Met
        435                 440
```

<210> 22
<211> 519
<212> PRT
<213> Zea mays

<400> 22

```
Met Leu Gly Val Gly Met Ala Ala Ala Val Leu Leu Gly Ala Val Ala
 1               5                  10                  15
Leu Leu Leu Ala Asp Ala Ala Ala Arg Arg Ala His Trp Trp Tyr Arg
            20                  25                  30
Glu Ala Ala Glu Ala Val Leu Val Gly Ala Val Ala Leu Val Val Val
        35                  40                  45
Asp Ala Ala Ala Arg Arg Ala His Gly Trp Tyr Arg Glu Ala Ala Leu
    50                  55                  60
Gly Ala Ala Arg Arg Ala Arg Leu Pro Pro Gly Glu Met Gly Trp Pro
65                  70                  75                  80
Leu Val Gly Gly Met Trp Ala Phe Leu Arg Ala Phe Lys Ser Gly Lys
                85                  90                  95
Pro Asp Ala Phe Ile Ala Ser Phe Val Arg Arg Phe Gly Arg Thr Gly
            100                 105                 110
Val Tyr Arg Ser Phe Met Phe Ser Ser Pro Thr Val Leu Val Thr Thr
        115                 120                 125
Ala Glu Gly Cys Lys Gln Val Leu Met Asp Asp Asp Ala Phe Val Thr
    130                 135                 140
Gly Trp Pro Lys Ala Thr Val Ala Leu Val Gly Pro Arg Ser Phe Val
145                 150                 155                 160
Ala Met Pro Tyr Asp Glu His Arg Arg Ile Arg Lys Leu Thr Ala Ala
                165                 170                 175
Pro Ile Asn Gly Phe Asp Ala Leu Thr Gly Tyr Leu Pro Phe Ile Asp
            180                 185                 190
Arg Thr Val Thr Ser Ser Leu Arg Ala Trp Ala Asp His Gly Gly Ser
        195                 200                 205
Val Glu Phe Leu Thr Glu Leu Arg Arg Met Thr Phe Lys Ile Ile Val
    210                 215                 220
Gln Ile Phe Leu Gly Gly Ala Asp Gln Ala Thr Thr Arg Ala Leu Glu
225                 230                 235                 240
Arg Ser Tyr Thr Glu Leu Asn Tyr Gly Met Arg Ala Met Ala Ile Asn
                245                 250                 255
Leu Pro Gly Phe Ala Tyr Arg Gly Ala Leu Arg Ala Arg Arg Arg Leu
            260                 265                 270
Val Ala Val Leu Gln Gly Val Leu Asp Glu Arg Arg Ala Ala Arg Ala
        275                 280                 285
Lys Gly Val Ser Gly Gly Gly Val Asp Met Met Asp Arg Leu Ile Glu
    290                 295                 300
Ala Gln Asp Glu Arg Gly Arg His Leu Asp Asp Asp Glu Ile Ile Asp
305                 310                 315                 320
Val Leu Val Met Tyr Leu Asn Ala Gly His Glu Ser Ser Gly His Ile
                325                 330                 335
Thr Met Trp Ala Thr Val Phe Leu Gln Glu Asn Pro Asp Met Phe Ala
            340                 345                 350
Arg Ala Lys Ala Glu Gln Glu Ala Ile Met Arg Ser Ile Pro Ser Ser
        355                 360                 365
Gln Arg Gly Leu Thr Leu Arg Asp Phe Arg Lys Met Glu Tyr Leu Ser
    370                 375                 380
Gln Val Ile Asp Glu Thr Leu Arg Leu Val Asn Ile Ser Phe Val Ser
385                 390                 395                 400
Phe Arg Gln Ala Thr Arg Asp Val Phe Val Asn Gly Tyr Leu Ile Pro
                405                 410                 415
Lys Gly Trp Lys Val Gln Leu Trp Tyr Arg Ser Val His Met Asp Pro
            420                 425                 430
Gln Val Tyr Pro Asp Pro Thr Lys Phe Asp Pro Ser Arg Trp Glu Gly
        435                 440                 445
```

```
His Ser Pro Arg Ala Gly Thr Phe Leu Ala Phe Gly Leu Gly Ala Arg
    450                 455                 460
Leu Cys Pro Gly Asn Asp Leu Ala Lys Leu Glu Ile Ser Val Phe Leu
465                 470                 475                 480
His His Phe Leu Leu Gly Tyr Lys Leu Ala Arg Thr Asn Pro Arg Cys
                485                 490                 495
Arg Val Arg Tyr Leu Pro His Pro Arg Pro Val Asp Asn Cys Leu Ala
            500                 505                 510
Lys Ile Thr Arg Val Gly Ser
        515
```

<210> 23
<211> 492
<212> PRT
<213> Danio rerio

<400> 23

```
Met Gly Leu Tyr Thr Leu Met Val Thr Phe Leu Cys Thr Ile Val Leu
 1               5                  10                  15
Pro Val Leu Leu Phe Leu Ala Ala Val Lys Leu Trp Glu Met Leu Met
            20                  25                  30
Ile Arg Arg Val Asp Pro Asn Cys Arg Ser Pro Leu Pro Pro Gly Thr
        35                  40                  45
Met Gly Leu Pro Phe Ile Gly Glu Thr Leu Gln Leu Ile Leu Gln Arg
    50                  55                  60
Arg Lys Phe Leu Arg Met Lys Arg Gln Lys Tyr Gly Cys Ile Tyr Lys
65                  70                  75                  80
Thr His Leu Phe Gly Asn Pro Thr Val Arg Val Met Gly Ala Asp Asn
                85                  90                  95
Val Arg Gln Ile Leu Leu Gly Glu His Lys Leu Val Ser Val Gln Trp
            100                 105                 110
Pro Ala Ser Val Arg Thr Ile Leu Gly Ser Asp Thr Leu Ser Asn Val
        115                 120                 125
His Gly Val Gln His Lys Asn Lys Lys Lys Ala Ile Met Arg Ala Phe
    130                 135                 140
Ser Arg Asp Ala Leu Glu His Tyr Ile Pro Val Ile Gln Gln Glu Val
145                 150                 155                 160
Lys Ser Ala Ile Gln Glu Trp Leu Gln Lys Asp Ser Cys Val Leu Val
                165                 170                 175
Tyr Pro Glu Met Lys Lys Leu Met Phe Arg Ile Ala Met Arg Ile Leu
            180                 185                 190
Leu Gly Phe Glu Pro Glu Gln Ile Lys Thr Asp Glu Gln Glu Leu Val
        195                 200                 205
Glu Ala Phe Glu Glu Met Ile Lys Asn Leu Phe Ser Leu Pro Ile Asp
    210                 215                 220
Val Pro Phe Ser Gly Leu Tyr Arg Gly Leu Arg Ala Arg Asn Phe Ile
225                 230                 235                 240
His Ser Lys Ile Glu Glu Asn Ile Arg Lys Lys Ile Gln Asp Asp Asp
                245                 250                 255
Asn Glu Asn Glu Gln Lys Tyr Lys Asp Ala Leu Gln Leu Leu Ile Glu
            260                 265                 270
Asn Ser Arg Arg Ser Asp Glu Pro Phe Ser Leu Gln Ala Met Lys Glu
        275                 280                 285
Ala Ala Thr Glu Leu Leu Phe Gly Gly His Glu Thr Thr Ala Ser Thr
    290                 295                 300
Ala Thr Ser Leu Val Met Phe Leu Gly Leu Asn Thr Glu Val Val Gln
305                 310                 315                 320
```

```
Lys Val Arg Glu Glu Val Gln Glu Lys Val Glu Met Gly Met Tyr Thr
                325                 330                 335
Pro Gly Lys Gly Leu Ser Met Glu Leu Leu Asp Gln Leu Lys Tyr Thr
            340                 345                 350
Gly Cys Val Ile Lys Glu Thr Leu Arg Ile Asn Pro Pro Val Pro Gly
        355                 360                 365
Gly Phe Arg Val Ala Leu Lys Thr Phe Glu Leu Asn Gly Tyr Gln Ile
    370                 375                 380
Pro Lys Gly Trp Asn Val Ile Tyr Ser Ile Cys Asp Thr His Asp Val
385                 390                 395                 400
Ala Asp Val Phe Pro Asn Lys Glu Glu Phe Gln Pro Glu Arg Phe Met
                405                 410                 415
Ser Lys Gly Leu Glu Asp Gly Ser Arg Phe Asn Tyr Ile Pro Phe Gly
            420                 425                 430
Gly Gly Ser Arg Met Cys Val Gly Lys Glu Phe Ala Lys Val Leu Leu
        435                 440                 445
Lys Ile Phe Leu Val Glu Leu Thr Gln His Cys Asn Trp Ile Leu Ser
    450                 455                 460
Asn Gly Pro Pro Thr Met Lys Thr Gly Pro Thr Ile Tyr Pro Val Asp
465                 470                 475                 480
Asn Leu Pro Thr Lys Phe Thr Ser Tyr Val Arg Asn
                485                 490
```

<210> 24
<211> 504
<212> PRT
<213> Homo sapiens

<400> 24

```
Met Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala
 1               5                  10                  15
Val Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu
            20                  25                  30
Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly
        35                  40                  45
Asn Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys
    50                  55                  60
His Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro
65                  70                  75                  80
Val Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Leu Val Leu Val Lys
                85                  90                  95
Glu Cys Tyr Ser Val Phe Thr Asn Arg Glu Pro Phe Gly Pro Val Gly
            100                 105                 110
Phe Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg
        115                 120                 125
Leu Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
    130                 135                 140
Met Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu
145                 150                 155                 160
Arg Arg Glu Arg Glu Thr Gly Lys Pro Val Thr Leu Lys Asp Val Phe
                165                 170                 175
Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Ser Ser Phe Gly Val Asn
            180                 185                 190
Val Asp Ser Leu Asn Asn Pro Gln Asp Pro Leu Val Glu Asn Thr Lys
        195                 200                 205
Lys Leu Leu Arg Phe Asp Phe Leu Asp Pro Phe Phe Leu Ser Ile Thr
    210                 215                 220
```

```
Val Phe Pro Phe Leu Ile Pro Ile Leu Glu Val Leu Asn Ile Cys Val
225                 230                 235                 240
Phe Pro Arg Glu Val Thr Asn Phe Leu Arg Lys Ala Val Lys Arg Met
                245                 250                 255
Lys Glu Ser Arg Leu Glu Asp Thr Gln Lys His Arg Val Asp Phe Leu
            260                 265                 270
Gln Leu Met Ile Asp Ser His Lys Asn Ser Lys Glu Thr Glu Ser His
        275                 280                 285
Lys Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile
    290                 295                 300
Phe Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Met Tyr
305                 310                 315                 320
Glu Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile
                325                 330                 335
Asp Ala Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu
            340                 345                 350
Gln Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe
        355                 360                 365
Pro Ile Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile
    370                 375                 380
Asn Gly Met Phe Ile Pro Lys Gly Trp Val Val Met Ile Pro Ser Tyr
385                 390                 395                 400
Ala Leu His Arg Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Leu
                405                 410                 415
Pro Glu Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile
            420                 425                 430
Tyr Thr Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe
        435                 440                 445
Ala Leu Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe
    450                 455                 460
Ser Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Leu
465                 470                 475                 480
Gly Gly Leu Leu Gln Pro Glu Lys Pro Val Val Leu Lys Val Glu Ser
                485                 490                 495
Arg Asp Gly Thr Val Ser Gly Ala
            500
```

<210> 25
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(575)
<223> Xaa = Any Amino Acid or No Amino Acid

<400> 25

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Ser Xaa Xaa Ala Leu Xaa Val Xaa
        35                  40                  45
Leu Xaa Leu Ala Ala Arg Arg Xaa Xaa Xaa Arg Tyr Xaa Xaa Xaa Xaa
```

```
    50                  55                  60
Xaa Xaa Xaa Xaa Arg Arg Lys Xaa Leu Pro Pro Gly Thr Met Gly Leu
65                  70                  75                  80
Pro Xaa Leu Gly Glu Thr Leu Gln Phe Leu Lys Xaa Xaa Xaa Xaa Xaa
                85                  90                  95
Xaa Pro Gly Asp Phe Xaa Lys Glu Arg Val Xaa Xaa Tyr Gly Xaa Xaa
            100                 105                 110
Xaa Xaa Ile Tyr Lys His Leu Phe Gly Glu Pro Thr Ile Xaa Ser Xaa
        115                 120                 125
Asp Ala Glu Leu Asn Arg Phe Xaa Leu Xaa Asn Glu Gly Xaa Lys Leu
    130                 135                 140
Phe Xaa Cys Xaa Xaa Pro Ala Ser Xaa Xaa Gly Xaa Leu Gly Lys Xaa
145                 150                 155                 160
Ser Leu Xaa Ala Xaa Xaa Gly Xaa Glu His Lys Arg Met Arg Xaa Leu
                165                 170                 175
Leu Xaa Ser Xaa Phe Ser Xaa Xaa Xaa Xaa Leu Asp His Xaa Leu Pro
            180                 185                 190
Xaa Ile Asp Arg Xaa Val Arg Ser Xaa Leu Xaa Xaa Trp Xaa Xaa Xaa
        195                 200                 205
Xaa Gln Lys Xaa Xaa Ile Val Xaa Xaa Xaa Xaa Glu Xaa Lys Lys Met
    210                 215                 220
Thr Phe Asp Xaa Xaa Xaa Lys Xaa Xaa Met Gly Xaa Xaa Pro Xaa Xaa
225                 230                 235                 240
Glu Xaa Thr Xaa Xaa Xaa Xaa Leu Val Xaa Glu Xaa Glu Xaa Leu Ile
                245                 250                 255
Lys Gly Leu Phe Ser Leu Pro Ile Asn Leu Pro Xaa Thr Ala Tyr Xaa
            260                 265                 270
Lys Ala Leu Xaa Ala Arg Ala Phe Xaa Xaa Ala Xaa Leu Glu Xaa Xaa
        275                 280                 285
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Glu Xaa Arg Xaa Glu Glu
    290                 295                 300
Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305                 310                 315                 320
Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Leu Leu Gly Leu Leu Xaa Ala Xaa
                325                 330                 335
Xaa Xaa Xaa Xaa Xaa Glu Asp Glu Xaa Xaa Xaa Xaa Leu Ser Asp Xaa
            340                 345                 350
Glu Ile Xaa Asp Xaa Ile Xaa Xaa Leu Leu Phe Ala Gly His Glu Thr
        355                 360                 365
Thr Ser Ser Xaa Leu Xaa Xaa Ala Val Lys Phe Leu Xaa Glu His Pro
    370                 375                 380
Asp Val Xaa Glu Xaa Leu Arg Glu Glu His Xaa Ala Ile Xaa Arg Ala
385                 390                 395                 400
Lys Lys Xaa Xaa Xaa Glu Ser Xaa Leu Thr Xaa Xaa Asp Tyr Lys Lys
                405                 410                 415
Met Xaa Tyr Thr Xaa Cys Val Ile Asn Glu Thr Leu Arg Leu Ala Xaa
            420                 425                 430
Ile Val Gly Gly Xaa Phe Arg Xaa Ala Xaa Lys Asp Val Glu Ile Asn
        435                 440                 445
Gly Tyr Xaa Ile Pro Lys Gly Trp Lys Val Xaa Tyr Ser Ile Arg Ala
    450                 455                 460
Val His Leu Asp Pro Asp Xaa Tyr Pro Asp Pro Glu Lys Phe Asn Pro
465                 470                 475                 480
Xaa Arg Trp Xaa Xaa Lys Xaa Xaa Xaa Xaa Ser Asn Ser Xaa Xaa Xaa
                485                 490                 495
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Pro Phe Gly Gly Gly Pro
            500                 505                 510
```

```
Arg Leu Cys Pro Gly Lys Glu Leu Ala Lys Leu Glu Met Xaa Val Phe
        515                 520                 525
Leu His Arg Leu Val Gln Xaa Phe Trp Glu Leu Ala Xaa Xaa Xaa Asp
    530                 535                 540
Xaa Xaa Xaa Lys Leu Val Xaa Phe Pro Thr Xaa Arg Pro Xaa Asp Asn
545                 550                 555                 560
Leu Pro Ile Lys Val Xaa Xaa Arg Asp Xaa Xaa Xaa Xaa Xaa Xaa
                565                 570                 575
```